KEMENTERIAN PERDAGANGAN DALAM NEGERI
DAN HAL EHWAL PENGGUNA MALAYSIA,
BAHAGIAN HARTA INTELEK,
TINGKAT 27, 30 DAN 32,
MENARA DAYABUMI,
JALAN SULTAN HISHAMUDDIN,
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Ministry of Domestic Trade and Consumer Affairs Malaysia,
Intellectual Property Division

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PATENT APPLICATION NO: PI 2000 4837

This is to certify that annexed hereto is a true copy from the records of the Registry of Trade Marks and Patents, Malaysia of the application as originally filed which is identified therein.

By authority of the
REGISTRAR OF PATENTS

[redacted]

ABDUL RAHMAN RAMLI
(CERTIFYING OFFICER)
15 August 2001

KEMENTERIAN PERDAGANGAN DALAM NEGERI
DAN HAL EHWAL PENGGUNA MALAYSIA
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Ministry of Domestic Trade and Consumer Affairs Malaysia
Intellectual Property Division.

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CERTIFICATE OF FILING

APPLICANT	:	UNIVERSITI PUTRA MALAYSIA
APPLICATION NO.	:	PI 20004837
REQUEST RECEIVED ON	:	16/10/2000
FILING DATE	:	16/10/2000
AGENT'S/APPLICANT'S FILE REF.	:	ISD 426/13/1 [EPD/2000-5/27]

Please find attached, a copy of the Request Form relating to the above application, with the filing date and application number marked thereon in accordance with Regulation 25(1).

Date : 20/10/2000

.....
(Hasnon Bt. Alang Mohd Rashid)
for Registrar of Patents

To : **DR. MARGARET CHAI SOOK YIN,**
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40911 SHAH ALAM,
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MALAYSIA.

FF 09

Patents Form No. 1
PATENTS ACT 1983

REQUEST FOR GRANT OF PATENT
[Regulations 7(1)]

To : The Registrar of Patents
Patent Registration Office
Kuala Lumpur,
Malaysia

For Official Use

APPLICATION RECEIVED NO. :

Fee received on:

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Applicant's Reference :

ISD 426/13/1 [EPD/2000-5/27]

THE APPLICANT(S) REQUEST(S) THE GRANT OF A PATENT IN RESPECT OF THE FOLLOWING PARTICULARS

I. TITLE OF INVENTION : Nucleotide Sequences of the Nucleocapsid (NP) and Phosphoprotein (P) Genes of a Malaysian Velogenic Newcastle Disease Virus Strain AF 2240 and the Production of the NP and P Proteins in *Escherichia coli*

II. APPLICANT(s) the data concerning each applicant must appear in this box or, if the space is insufficient, in the space below)

Name : UNIVERSITI PUTRA MALAYSIA

I.C./Passport No. : -

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* Permanent residence or principal place of business :

- as above -

Telephone Number
(if any)

03-5446129/
03-5446134

Fax Number
(if any)

03-5446146

SIRIM BERHAD DITERIMA 16 OCT 2000 Unit Pentadbiran Bahagian Harta Intelek

Additional Information (if any)

III. INVENTOR

Applicant is the inventor Yes [ ] No [✓]

If the applicant is not the inventor :

Name of inventor s: 1. Prof. Madya Datin Dr. Khatijah Yusoff
2. Dr. Tan Wen Siang
3. Cik Kho Chiew Ling

Address of inventors : Jabatan Biokimia dan Mikrobiologi,
Fakulti Sains dan Pengajian Alam Sekitar,
Universiti Putra Malaysia,
UPM 43400 Serdang, Selangor.

A statement justifying the applicant's right to the patent accompanies this Form :

Yes [✓] No [ ]

Additional Information (if any)

IV. AGENT OR REPRESENTATIVE

Applicant has appointed a patent agent in accompanying Form No. 17

Yes [✓]
No [ ]

Agent's Registration No. : (PA/2000/0099)

Applicants have appointed _____
To be their common representative

V. DIVISIONAL APPLICATION

This application is a divisional application [ ]

The benefit of the

filing date priority date [ ]

of the initial application is claimed in as much as the subject-matter of the present application is contained in the initial application identified below :

Initial Application No. : _____

Date of filing of initial application : _____

VI. DISCLOSURE TO BE DISREGARDED FOR PRIOR ART PURPOSES

Additional information is contained in supplemental box :

(a) Disclosure was due to acts of applicant or his predecessor in title ☐

Date of disclosure: _____

(b) Disclosure was due to abuse of rights of applicant or his predecessor in title ☐

Date of disclosure: _____

A statement specifying in more detail the facts concerning the disclosure accompanies this Form

Yes ☐

No ☐

Additional Information (If any)

VII. PRIORITY CLAIM (if any)

The priority of an earlier application is claimed as follows :

Country (if the earlier application is a regional or international application, indicate the office with Which it is filed) :

_____

Filing Date : _____

Application No. : _____

Symbol of the International Patent Classification :

If not yet allocated, please tick ☐

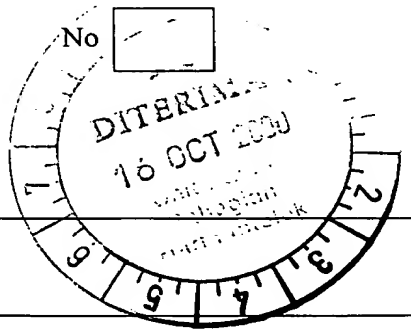
The priority of more than one earlier application is claimed:

Yes ☐ No ☐

The certified copy of the earlier application(s) accompanies this Form:

Yes ☐ No ☐

If No, it will be furnished by



Additional Information (if any)

20004837

VIII. CHECK LIST

A. This application contains the following :

1. request		Sheets
2. description	20	Sheets
3. claim	11	Sheets
4. abstract	1	Sheets
5. drawings	2	Sheets
Total	34	Sheets

B. This Form, as filed, is accompanied by the items checked below :

(a) signed Form No. 17	✓
(b) declaration that inventor does not wish to be named in the patent	
(c) statement justifying applicant's right to the patent	✓
(d) statement that certain disclosures to be disregarded	
(e) priority document (certified copy of earlier application)	
(f) cash, cheque, money order, banker's draft or postal order for the payment of application fee	✓
(g) other documents (specify) Form 5	✓

IX. SIGNATURE _____ 14/10/2000

Dr. Margaret Chai Sook Yin (Date)

**(~~Applicant~~/Agent)

If Agent, indicate Agent's Registration No. : (PA/2000/0099)

For Official Use

1. Date application received :

2. Date of receipt of correction, later filed papers or drawings completing the application :

* Delete whichever does not apply

** Type name under signature and delete whichever does not apply

PNMB., K.L.

Nucleotide Sequences of the Nucleocapsid (NP) and Phosphoprotein (P) Genes of a Malaysian Velogenic Newcastle Disease Virus Strain AF2240 and the Production of the NP and P Proteins in *Escherichia coli*

Field of the Invention

The present invention relates to nucleotide sequences encoding the nucleocapsid (NP) protein and phosphoprotein (P) of Newcastle disease virus (NDV) strain AF2240, and the production of the corresponding proteins with recombinant plasmids bearing the nucleotide sequences in *Escherichia coli*.

Description of the Prior Art

Newcastle disease virus (NDV) is the prototype of avian paramyxovirus, which causes a highly contagious disease known as Newcastle disease (ND) in many avian species. This disease is of great economic importance requiring control by vaccination or quarantine with slaughter of all birds in confirmed outbreaks, resulting in substantial losses in the poultry industry worldwide. Therefore, development of an improved vaccine and also a rapid and sensitive diagnostic test are greatly desired by the poultry industry.

A Malaysian heat resistant NDV strain AF2240, which causes 100% mortality in susceptible chicken flocks has been reported by Abdul Rahman *et al.* (1976) and Lai, C.M. (1985). Further studies by Idris *et al.* (1993) revealed that the thermostabilities of haemagglutination and neuraminidase activities of this AF2240 strain were found to be higher than those of other strains. The basis giving rise to these unique features is still unknown. However a comprehensive understanding of the viral proteins would provide some solutions and useful information for the development of heat stable recombinant vaccines and diagnostic tests.

The genome of NDV is a linear, non-segmented, single-stranded negative sense RNA with a molecular weight of 5.2-5.7x10^6 Daltons, or approximately 15,000 bases which encodes six main structural proteins. The genomic RNA is associated with the nucleocapsid (NP), phosphoprotein (P) and large (L) proteins. These macromolecules

form the transcriptive complex of the virus, which in turn is surrounded by a lipid bilayer membrane derived from the host cell. Embedded in the membrane are the haemagglutinin-neuraminidase (HN) and fusion (F) glycoproteins. Beneath the lipid bilayer is a shell of protein known as the matrix (M) protein, which is believed to interact with the transcriptive complex. The HN and F glycoproteins are associated with the host cell receptor during infection. The NP encapsidates the viral RNA together with the L protein which is thought to be the transcriptase, and a P protein with an unknown reason.

The genes encoding for the HN (EMBL/Gen Bank/DDBJ accession No.X70092), F (EMBL/Gen Bank/DDBJ accession No.AFO48763) and M (EMBL/Gen Bank/DDBJ accession No. AF060563) proteins of the NDV strain AF2240 have been completely sequenced by Tan *et al.* (1995), Salih *et al.* (2000) and Jemain, S.F.P. (1999) respectively. From the HN gene sequence of strain AF2240, it was quite clear that this strain is different from the other published NDV strains. The HN protein lacked the Arg (403) residue and contained 581 amino acids. At the time when the project was initiated, there was no information available on the coding sequences for the NP and P proteins of NDV strain AF2240. Therefore it remained a problem to prepare cDNA for the cloning of the NP and P genes of NDV.

The inventors have now successfully determined the nucleotide sequences encoding the NP and P proteins of NDV strain AF2240. The accession numbers for the genes encoding the NP and P proteins are EMBL/Gen Bank/DDBJ No. AF284646 and AF284647 respectively. The inventors had discovered that the proteins, in either non-fusion or fusion forms bearing the *myc* epitope and six residues of His at their carboxyl terminal end could be successfully produced in *E. coli* by means of recombinant DNA technologies. The NP and P proteins were expressed to a substantial level in the bacteria and can be recognised by chicken anti-NDV serum.

Summary of invention

The present invention provides nucleotides encoding the full length NP and P polypeptides of Newcastle disease virus strain AF2240. Whereas the genome of NDV is of length approximately 15,000 nucleotides, it has been determined, by this invention, that the portion coding for the NP polypeptide is approximately 1470 nucleotides long and the

portion that codes for the P polypeptide is approximately 1188 nucleotides long. Accordingly, one aspect of the present invention provides for the coding regions of the nucleocapsid (NP) and phosphoprotein (P) genes of Newcastle disease virus strain AF2240. Both the nucleotide sequences are as listed below:

NP coding region

```
        10         20         30         40         50         60
ATGTCTTCCG TATTCGATGA ATACGAGCAG CTCCTCGCTG CTCAGACTCG CCCCAATGGA

        70         80         90        100        110        120
GCTCACGGAG GGGGAGAGAG AGGGAGCACT TTAAGAGTTG AGGTCCCAGT ATTCACTCTT

       130        140        150        160        170        180
AACAGTGACG ATCCAGAAGA TAGATGGAAT TTTGCGGTAT TCTGTCTTCG GATTGCTGTT

       190        200        210        220        230        240
AGCGAGGACG CCAACAAACC GCTCAGGCAA GGTGCTCTCA TATCCCTCCT GTGCTCCCAT

       250        260        270        280        290        300
TCTCAAGTGA TGAGGAACCA TGTTGCCCTT GCAGGAAAAC AGAATGAGGC TACACTGACT

       310        320        330        340        350        360
GTTCTTGAGA TCGATGGTTT TACCAGCAGC GTGCCTCAGT TCAACAACAG GAGTGGGGTG

       370        380        390        400        410        420
TCTGAGGAGA GAGCACAGAG ATTCATGGTG ATAGCAGGGT CTCTCCCTCG GGCGTGCAGT

       430        440        450        460        470        480
AACGGTACTC CGTTCGTCAC GGCTGGGGTT GAAGATGATG CACCAGAAGA TATCACTGAT

       490        500        510        520        530        540
ACTCTGGAAA GAATCCTGTC TATCCAGGCT CAGGTATGGG TCACAGTAGC GAAGGCCATG

       550        560        570        580        590        600
ACTGCATATG AGACAGCAGA TGAGTCGGAA ACAAGAAGAA TCAATAAGTA CATGCAGCAA

       610        620        630        640        650        660
GGCAGAGTCC AGAAGAAGTA CATCCTCCAC CCTGTATGCA GGAGTGCAAT TCAACTCACA
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```
       670        680        690        700        710        720
ATCAGACATT CTCTGGCAGT CCGCATTTTC TTAGTTAGCG AGCTTAAGAG AGGCCGCAAT

       730        740        750        760        770        780
ACGGCAGGTG GGAGCTCCAC GTATTACAAC TTAGTAGGGG ATGTAGACTC ATACATCAGG

       790        800        810        820        830        840
AACACCGGAC TTACTGCATT CTTCCTTACA CTCAAATATG GAATTAATAC CAAGACATCA

       850        860        870        880        890        900
GCCCTAGCAC TCAGCAGCCT CACAGGCGAT ATCCAAAAGA TGAAGCAGCT CATGCGTTTA

       910        920        930        940        950        960
TATCGGATGA AGGGAGAAAA TGCGCCGTAC ATGACATTGC TAGGTGACAG TGATCAGATG

       970        980        990       1000       1010       1020
AGCTTTGCAC CGGCTGAGTA TGCACAGCTT TATTCTTTTG CCATGGGCAT GGCATCAGTC

      1030       1040       1050       1060       1070       1080
TTAGATAAAG GAACTGGCAA ATACCAATTC GCCAGAGACT TCATGAGCAC ATCATTCTGG

      1090       1100       1110       1120       1130       1140
AGACTCGGGG TGGAGTATGC TCAGGCTCAG GGGAGTAGCA TCAACGAAGA CATGGCTGCT

      1150       1160       1170       1180       1190       1200
GAGCTAAAAC TAACCCCGGC AGCAAGAAGG GGCCTGGCAG CTGCTGCCCA ACGAGTGTCT

      1210       1220       1230       1240       1250       1260
GAGGAAACTG GCAGCGTGGA TATTCCTACT CAACAAGCCG GGGTCCTCAC TGGGCTCAGC

      1270       1280       1290       1300       1310       1320
GATGGAGGCC CCCGAGCCTC TCAGGGTGGA TCGAACAAGT CGCAAGGGCA ACCAGATGCC

      1330       1340       1350       1360       1370       1380
GGAGATGGGG AGACCCAATT CTTGGATTTG ATGAGAGCAG TGGCGAACAG CATGCGAGAA

      1390       1400       1410       1420       1430       1440
GCGCCAAACT CCGCACAGAG CACCACCCAC CCGGAACCCC CCCCGACTCC CGGGCCATCA
```

```
      1450        1460        1470        1480        1490        1500
CAAGATAACG ACACCGACTG GGGGTATTGA ..........  ..........  ..........
```

P gene coding region

```
        10          20          30          40          50          60
ATGGCCACCT TTACAGATGC GGAGATAGAT GATATATTTG AGACCAGTGG AACTGTCATT

        70          80          90         100         110         120
GACAGCATAA TTACGGCCCA GGGTAAATCA GCAGAGACTG TCGGAAGGAG CGCAATCCCA

       130         140         150         160         170         180
CAAGGCAAGA CCAAAGCGCT GAGCATAGCA TGGGAGAAGC ATGGGAGCAT CCAACCATCC

       190         200         210         220         230         240
ACCAGCCAGG ACAACCCCGA CCAACAGGAT AGACCAGACA AACAGCTATC CACACCTGAG

       250         260         270         280         290         300
CAGGCGACCC CACACAACAG CTCGCCAGCC ACATCCGCCG AACCGCTCCC CACTCAGGCC

       310         320         330         340         350         360
GCAGGTGAGG CCGGCGACAC ACAGCTCAAG ACCGGAGCAA GCAACTCTCT TCTGTCTATG

       370         380         390         400         410         420
CTCGACAAGC TGAGCAATAA ACCATCTAAT GCTAAAAAGG GCCCATGGTC GAGTCCCCAG

       430         440         450         460         470         480
GAAGGATATC ATCAACCTCC GACCCAACAA CATGGGGATC AGCCGAACCG CGGAAACAGC

       490         500         510         520         530         540
CAGGAGAGGC TGCGGCACCA AGCCAAGGCC GCCCCTGGAA GCCGGGGCAC AGACGCGAGC

       550         560         570         580         590         600
ACAGCATATC ATGGACAATG GAAGGAGTCA CAACTATCAG CTGGTGCAAC CCCTCATGTG

       610         620         630         640         650         660
CTCCAATCAG GGCAGAGCCA AGACAGTACT CCTGTACCTG TGGATCATGT CCAGCCACCT

       670         680         690         700         710         720
GTCGACTTTG TGCAGGCGAT GATGACTATG ATGGAGGCGT TATCACAGAA GGTAAGTAAA
```

```
          730         740         750         760         770         780
GTCGACTATC AGCTAGACCT AGTCTTAAAG CAGACATCCT CCATCCCTAT GATGCGGTCT

          790         800         810         820         830         840
GAAATCCAAC AGCTAAAAAC ATCTGTTGCG GTCATGGAAG CTAATTTAGG CATGATGAAA

          850         860         870         880         890         900
ATTCTGGACC CTGGTTGTGC TAACATTTCA TCCTTAAGTG ATCTGCGGGC AGTCGCCCGG

          910         920         930         940         950         960
TCCCACCCAG TTTTAATTTC AGGCCCCGGA GATCCGTCCC CCTACGTGAC ACAAGGGGGT

          970         980         990        1000        1010        1020
GAGATGACAC TCAATAAACT CTCACAACCA GTACAACACC CTTCCGAGTT AATTAAATCT

         1030        1040        1050        1060        1070        1080
GCCACAGCGG GCGGACCTGA TATGGGAGTG GAAAAGGACA CTGTCCGTGC ATTGATCACC

         1090        1100        1110        1120        1130        1140
TCGCGCCCGA TGCATCCAAG CTCCTCAGCT AAGCTCCTGA GTAAGCTGGA TGCAGCCGGG

         1150        1160        1170        1180        1190        1200
TCGATTGAAG AGATCAGAAA GATCAAGCGC CTTGCACTAA ATGGCTAA.. ..........
```

Further, the present invention provides the amino acid sequences of both the NP and P proteins as listed below:

NP gene: amino acid sequence

```
  1  M   S   S   V   F   D   E   Y   E   Q   L   L   A   A   Q   T      16
     ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
     1           10          20          30          40

 17  R   P   N   G   A   H   G   G   G   E   R   G   S   T   L   R      32
     CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
     50          60          70          80          90
```

```
33  V  E  V  P  V  F  T  L  N  S  D  D  P  E  D  R   48
    GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
      100        110        120        130        140

49  W  N  F  A  V  F  C  L  R  I  A  V  S  E  D  A   64
    TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
      150        160        170        180        190

65  N  K  P  L  R  Q  G  A  L  I  S  L  L  C  S  H   80
    AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
         200        210        220        230        240

81  S  Q  V  M  R  N  H  V  A  L  A  G  K  Q  N  E   96
    TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
            250        260        270        280

97  A  T  L  T  V  L  E  I  D  G  F  T  S  S  V  P  112
    GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
  290        300        310        320        330

113 Q  F  N  N  R  S  G  V  S  E  E  R  A  Q  R  F  128
    CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
      340        350        360        370        380

129 M  V  I  A  G  S  L  P  R  A  C  S  N  G  T  P  144
    ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG
      390        400        410        420        430

145 F  V  T  A  G  V  E  D  D  A  P  E  D  I  T  D  160
    TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT
         440        450        460        470        480

161 T  L  E  R  I  L  S  I  Q  A  Q  V  W  V  T  V  176
    ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA
            490        500        510        520

177 A  K  A  M  T  A  Y  E  T  A  D  E  S  E  T  R  192
    GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA
  530        540        550        560        570

193 R  I  N  K  Y  M  Q  Q  G  R  V  Q  K  K  Y  I  208
    AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC
      580        590        600        610        620
```

```
209  L  H  P  V  C  R  S  A  I  Q  L  T  I  R  H  S  224
     CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT
         630        640        650        660        670

225  L  A  V  R  I  F  L  V  S  E  L  K  R  G  R  N  240
     CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT
            680        690        700        710        720

241  T  A  G  G  S  S  T  Y  Y  N  L  V  G  D  V  D  256
     ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC
               730        740        750        760

257  S  Y  I  R  N  T  G  L  T  A  F  F  L  T  L  K  272
     TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA
   770        780        790        800        810

273  Y  G  I  N  T  K  T  S  A  L  A  L  S  S  L  T  288
     TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA
      820        830        840        850        860

289  G  D  I  Q  K  M  K  Q  L  M  R  L  Y  R  M  K  304
     GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG
         870        880        890        900        910

305  G  E  N  A  P  Y  M  T  L  L  G  D  S  D  Q  M  320
     GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG
            920        930        940        950        960

321  S  F  A  P  A  E  Y  A  Q  L  Y  S  F  A  M  G  336
     AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC
               970        980        990       1000

337  M  A  S  V  L  D  K  G  T  G  K  Y  Q  F  A  R  352
     ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA
  1010       1020       1030       1040       1050

353  D  F  M  S  T  S  F  W  R  L  G  V  E  Y  A  Q  368
     GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG
      1060       1070       1080       1090       1100

369  A  Q  G  S  S  I  N  E  D  M  A  A  E  L  K  L  384
     GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA
         1110       1120       1130       1140       1150
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```
385  T   P   A   A   R   R   G   L   A   A   A   A   Q   R   V   S   400
     ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT
           1160        1170        1180        1190        1200

401  E   E   T   G   S   V   D   I   P   T   Q   Q   A   G   V   L   416
     GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC
               1210        1220        1230        1240

417  T   G   L   S   D   G   G   P   R   A   S   Q   G   G   S   N   432
     ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC
   1250        1260        1270        1280        1290

433  K   S   Q   G   Q   P   D   A   G   D   G   E   T   Q   F   L   448
     AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG
     1300        1310        1320        1330        1340

449  D   L   M   R   A   V   A   N   S   M   R   E   A   P   N   S   464
     GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
       1350        1360        1370        1380        1390

465  A   Q   S   T   T   H   P   E   P   P   P   T   P   G   P   S   480
     GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
           1400        1410        1420        1430        1440

481  Q   D   N   D   T   D   W   G   Y   *                           490
     CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
               1450        1460        1470
```

P gene: amino acid sequence

```
1    M   A   T   F   T   D   A   E   I   D   D   I   F   E   T   S   16
     ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
     1           10          20          30          40

17   G   T   V   I   D   S   I   I   T   A   Q   G   K   S   A   E   32
     GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
     50          60          70          80          90

33   T   V   G   R   S   A   I   P   Q   G   K   T   K   A   L   S   48
     ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
       100         110         120         130         140
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49  I  A  W  E  K  H  G  S  I  Q  P  S  T  S  Q  D  64
   ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
       150        160        170        180        190

65  N  P  D  Q  Q  D  R  P  D  K  Q  L  S  T  P  E  80
   AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
          200        210        220        230        240

81  Q  A  T  P  H  N  S  S  P  A  T  S  A  E  P  L  96
   CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
             250        260        270        280

97  P  T  Q  A  A  G  E  A  G  D  T  Q  L  K  T  G  112
   CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
290        300        310        320        330

113 A  S  N  S  L  L  S  M  L  D  K  L  S  N  K  P  128
   GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
    340        350        360        370        380

129 S  N  A  K  K  G  P  W  S  S  P  Q  E  G  Y  H  144
   TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
       390        400        410        420        430

145 Q  P  P  T  Q  Q  H  G  D  Q  P  N  R  G  N  S  160
   CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
          440        450        460        470        480

161 Q  E  R  L  R  H  Q  A  K  A  A  P  G  S  R  G  176
   CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
             490        500        510        520

177 T  D  A  S  T  A  Y  H  G  Q  W  K  E  S  Q  L  192
   ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA
530        540        550        560        570

193 S  A  G  A  T  P  H  V  L  Q  S  G  Q  S  Q  D  208
   TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC
    580        590        600        610        620

209 S  T  P  V  P  V  D  H  V  Q  P  P  V  D  F  V  224
   AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG
       630        640        650        660        670
```

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225  Q   A   M   M   T   M   M   E   A   L   S   Q   K   V   S   K   240
     CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA
             680         690         700         710         720
241  V   D   Y   Q   L   D   L   V   L   K   Q   T   S   S   I   P   256
     GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT
             730         740         750         760

257  M   M   R   S   E   I   Q   Q   L   K   T   S   V   A   V   M   272
     ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG
         770         780         790         800         810

273  E   A   N   L   G   M   M   K   I   L   D   P   G   C   A   N   288
     GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC
           820         830         840         850         860

289  I   S   S   L   S   D   L   R   A   V   A   R   S   H   P   V   304
     ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT
           870         880         890         900         910

305  L   I   S   G   P   G   D   P   S   P   Y   V   T   Q   G   G   320
     TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
             920         930         940         950         960

321  E   M   T   L   N   K   L   S   Q   P   V   Q   H   P   S   E   336
     GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
             970         980         990         1000

337  L   I   K   S   A   T   A   G   G   P   D   M   G   V   E   K   352
     TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
       1010        1020        1030        1040        1050

353  D   T   V   R   A   L   I   T   S   R   P   M   H   P   S   S   368
     GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
           1060        1070        1080        1090        1100

369  S   A   K   L   L   S   K   L   D   A   A   G   S   I   E   E   384
     TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
           1110        1120        1130        1140        1150

385  I   R   K   I   K   R   L   A   L   N   G   *                   396
     ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
             1160        1170        1180
```

A primary use of the nucleotides as defined above is for the creation of plasmids using recombinant DNA technologies. The resulting recombinant molecule can then be introduced into an appropriate host. The plasmids thus created can be used to encode NP and P proteins. For expression of the NP and P proteins, any of the common expression vectors, especially the bacterial vectors can be used. The usable bacterial hosts for the vectors include any of the conventional prokaryotic cells. In this invention, the bacterial host used was *Escherichia coli*. Accordingly, a further aspect of the present invention provides for a prokaryotic cell, such as for example a bacterial cell and in particular an *E. coli* cell containing the nucleotides as defined above for the production of NP and P proteins.

The NP and P proteins, produced using recombinant plasmids in accordance with the present invention, can be in the fusion or non-fusion forms. In accordance with the embodiment of the present invention, it provides a method for producing the fusion and non-fusion forms of both the NP and P proteins of NDV virus strain AF2240 in an *E. coli* system. The preferred method for producing the fusion and non-fusion forms of both the NP and P proteins of NDV virus strain AF2240 comprises culturing the transformed *E. coli* of the present invention on an appropriate medium to express the said nucleocapsid protein and phosphoprotein, and isolating and purifying the expressed fusion proteins from the cultures.

While the invention will now be described in connection with certain preferred embodiments in the following experiments so that aspects thereof may be more fully understood and appreciated, it is not intended to limit the invention to these particular embodiments. On the contrary, it is intended to cover all alternatives, modifications and equivalents as may be included within the scope of the invention as defined by the appended claims.

Brief description of the figures

Figure 1 is a western blot of NDV nucleocapsid protein (NP) expressed by transformed *E. coli* TOP10 containing plasmid pTrcHis2-NP

Figure 2 is a western blot of NDV phosphoprotein (P) expressed by transformed *E. coli* TOP10 containing plasmid pTrcHis2-P

Detailed description of the invention

The present invention was accomplished through the employment of the recombinant DNA techniques which comprises the amplification of the NP and P coding regions of NDV strain AF2240, the cloning of the genes into the expression vector, the production of the transformed *E. coli*, the cultivation of the transformant, the expression of the NP and P proteins and the purification of the expressed fusion proteins.

The NP and P coding regions of NDV strain AF2240 which had been cloned into the expression vector were prepared through reverse transcription-polymerase chain reaction (RT-PCR). Three primers were used for each gene, which consisted of one forward and two reverse primers as listed below:

For the amplification of the NP gene

NPf1 (20 *mer*): 5'- cct tct gcc aac atg tct tc -3' (Forward primer)
NPr1 (20 *mer*): 5'- tca ata ccc cca gtc ggt gt -3' (Reverse primer)
NPr2 (18 *mer*): 5'- ata ccc cca gtc ggt gtc -3' (Reverse primer)

For the amplification of the P gene

Pf1 (20 *mer*): 5'- atg gcc acc ttt aca gat gc -3' (Forward primer)
Pr1 (23 *mer*): 5'- taa tta gcc att tag tgc aag gc -3' (Reverse primer)
Pr2 (21 *mer*): 5'- gcc att tag tgc aag gcg ctt -3' (Reverse primer)

Incorporation of primers designated as NPf1 and NPr1 (for the NP gene), or Pf1 and Pr1 (for the P gene) during PCR had amplified gene products containing a stop codon at their 3' ends, while the presence of primers NPf1 and NPr2 (for the NP gene) or Pf1 and Pr2 (for the P gene) gave rise to genes without any no stop codon. For cloning and expression purposes, a commercially available expression vector, pTrcHis2 (Invitrogen, USA) containing the coding regions for the *myc* epitope and 6 His residues downstream of the multiple cloning site was used. After cloning of the respective coding regions of NP and P genes into the pTrcHis2 vector, they were subsequently introduced into a bacterial host *E. coli* TOP10. The resulting plasmid harbouring the NP gene was designated as pTrcHis2-NP while the other one with the P gene as an insert was denoted as pTrcHis2-P. Both the

NP and P proteins were expressed in *E.coli* TOP10 cells as non-fusion and fusion proteins. The latter forms contain the *myc* epitope and 6 His residues at their C termini. For protein identification, protein samples were analysed with SDS- PAGE and then followed by immunoblotting with the anti-NDV chicken serum and the anti-*myc* monoclonal antibody. The western blots for NP and P proteins are as shown in Figure 1 and Figure 2, respectively.

The expressed NP fusion protein was purified with affinity chromatography (nickel column), and was judged to be more than 90% pure by SDS-PAGE.

The nucleotide sequences of the NP and P genes were determined by the ABI PRISM automated sequencer, model 377. The recombinant plasmids, pTrcHis2-NP and pTrcHis2-P, were used as templates and the synthetic primers used in the sequencing reactions of the NP and P genes are as follows:

<u>For the sequencing of the NP gene coding region</u>

pTrcHis2F (21 *mer*): 5'- gag gta tat att aat gta tcg -3'
sNPf1 (21 *mer*): 5'- gac tca tac atc agg aac acc -3'
sNPf2 (21 *mer*): 5'- gat gag agc agt ggc gaa cag -3'
pTrcHis2R (18 mer): 5'- gat tta atc tgt atc agg -3'
sNPr1 (20 *mer*): 5'- tca ata ccc cca gtc ggt gt -3'
sNPr2 (21 *mer*): 5'- cta agt tgt aat acg tgg agc -3'
sNPr3 (21 *mer*): 5'- cca tcg atc tca aga aca tgc -3'

<u>For the sequencing of the P gene coding region</u>

pTrcHis2F (21 *mer*): 5'- gag gta tat att aat gta tcg -3'
sPf1 (21 *mer*): 5'- gtc gac ttt gtg cag gcg atg -3'
sPf2 (21 *mer*): 5'- gga cac tgt ccg tgc att gat -3'
pTrcHis2.R (18 *mer*): 5'- gat tta atc tgt atc agg -3'
sPr1 (21 *mer*): 5'- cca ggg tcc aga att ttc atc -3'
sPr2 (22 *mer*): 5'- ggt gtg gat agc tgt ttg tct g -3'

Both the NP and P coding regions were sequenced from 5' to 3' direction and reversely from 3' to 5' direction.

Example I illustrates the recombinant DNA techniques employed in obtaining bacterial clones harbouring a plasmid containing inserts of NP and P coding cDNA for NDV genomic RNA, the nucleotide sequences of the NP and P genes, and also the expressed NP and P proteins.

EXAMPLE I

Virus Propagation

The stock of NDV strain AF2240 was originally obtained from the Veterinary Research Institute (VRI), Ipoh. The virus was grown in the allantoic cavity of 8 to 9 day-old chicken embryonated eggs according to the procedures of Blaskovic and Styk (1967). After 3 - 4 days of incubation at 37°C, the eggs were chilled overnight at 4°C. The allantoic fluid was then harvested and the presence of the viruses was determined by haemagglutination (HA) test. The allantoic fluid which showed positive reaction of HA test was then clarified by centrifugation at 6000 xg for 20 min at 4°C (Beckman, JA14 rotor, USA) to remove debris.

Genomic RNA extraction

Total RNA was extracted using the Trizol LS reagent (Gibco BRL, USA). Briefly, 250 µl of the virus infected allantoic fluid was mixed with 750 µl Trizol LS reagent and incubated for 5 min at room temperature. After incubation, 100 µl of 1-bromo-3-chloropropane (BCP) (MRC, UK) was added and the mixtures were mixed vigorously for about 15 s and again incubated at room temperature for 10 min. The mixtures were phase separated by microcentrifugating at 13,000 xg for 15 min at 4°C (Jouan MR 1812, France). The RNA was then precipitated by adding 500 µl of isopropanol (Merck) to the aqueous phase and left at room temperature for 10 min. The precipitated RNA was microcentrifuged at 13,000 xg for 10 min and the pellet obtained was washed once with 75% (v/v) diethyl pyrocarbonate (DEPC) (Sigma, USA) treated ethanol (Hamburg). The pellet was dissolved in 20 µl of DEPC treated dH_2O.

cDNA synthesis and amplification of nucleocapsid (NP) and phosprotein (P) genes by RT-PCR

The amplification reactions were carried out in a programmed thermal cycler (MJ Research Inc. USA). Synthesis of the first strand cDNA was performed in a final volume of 30 µl. The reaction mixture contained 0.4 µM of each the forward and reverse primers, 0.2 mM deoxynucleoside triphosphate (MBI Fermentas, Inc. USA), 5 U of AMV reverse transcriptase (Promega, USA), 8 U of RNase inhibitor (Gibco BRL, USA), 1.5 mM of $MgCl_2$ and 1x of reaction buffer (50 mM Tris-HCl, 15 mM $(NH_4)_2SO_4$, 0.1% Triton X-100). The mixture was incubated at 42°C for 30 min to synthesise the first strand of cDNA, and then 94°C for 3 min to inactivate the reverse transcriptase.

For the amplification of the respective NP and P genes, another 20 µl of reaction mixture containing 1 U of DyNAzyme EXT DNA polymerase (FINNZYMES), 1.5 mM of $MgCl_2$ and 1 x of reaction buffer was added to the top of the above cDNA mixture which was held at 94°C in the thermal cycler. The PCR profile for the amplification of NP gene comprising denaturation at 94°C for 30 s, annealing at 55°C for 50 s and extension at 72°C for 1 min for a total of 30 cycles. To ensure a complete synthesis of the PCR product, the extension step at 72°C was prolonged for 7 min after the last cycle. The PCR profile for the amplification of P gene was basically similar to that of NP gene, except the annealing step was carried out at 55°C for 30 s.

Purification of the amplified PCR products

A total of 40 µl of the amplified PCR product was analysed on 1% TAE agarose gel. After the staining with ethidium bromide, the band with the correct size was excised from the gel and purified with the Wizard PCR Preps DNA Purification System (Promega, USA) according to the manufacturer's procedures. After purification, 5 µl of the PCR product was again analysed with agarose gel electrophoresis to determine the recovery of the PCR product, which would be used in TA cloning.

TOPO TA Cloning of NP and P genes

Four µl of the purified NP or P DNA fragments carrying an A overhang at their 3' ends was mixed with 1 µl of the pTrcHis2 TOPO expression vector (Invitogen, USA) and the ligation reaction was carried out at room temperature (25°C) for 5 min to form the desired recombinant plasmid.

Transformation

For transformation, 5 µl of the ligation mixture was added to 50 µl of TOP10 *E. coli* competent cells (Invitrogen, USA). The transformation mixture was incubated on ice for 30 min and the cells were heated at 42°C for 30 to 60 s. This was followed by the adding of 250 µl SOC medium (2% trypton,0.5% yeast extract, 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$, 20 mM glucose) and the incubation of the reaction mixture at 37°C for 30 to 60 min with shaking at 250 rpm. Thirty-50 µl of the transformation mixture was spread on a LB plate containing 50 µg/ml ampicillin and 0.5% of glucose, and the plates were then incubated overnight at 37°C.

Screening for positive clones

Ten single colonies were randomly chosen and cultured overnight in 3 to 5 ml of LB medium containing 50 µg/ml ampicillin and 0.5% glucose. Plasmid DNA was isolated by using the alkaline lysis method and the orientation of the insert in the positive clones was confirmed by PCR.

Protein expression

The identified positive clones were cultured overnight in LB medium containing 50 µg/ml ampicillin. The next day, 10 ml of LB medium containing 50 µg/ml ampicillin was inoculated with 0.2 ml of the overnight culture and incubated at 37°C with shaking at 250 rpm. Once the cells reached the optical density of 0.6 to 0.8 at A_{600}, 1 mM IPTG was

added into the culture and continued shaking for 3 to 5 hours. The cells were harvested from the culture by centrifugation and then subjected to polyacrylamide gel electrophoresis (SDS-PAGE).

SDS-PAGE and western blotting

The cell pellets (from 1 ml culture solution) were resuspended in 50 to 100 µl of 1X SDS-PAGE sample buffer and boiled for 10 min. Five to 10 µl of the sample was loaded onto 12% SDS-PAGE gel and eletrophoresesed for 70 to 80 min at 32 volt. The proteins on SDS-PAGE gel were then electro-transferred onto a nitrocellulose membrane for 1 h. Western blotting was carried out by blocking the membrane first with skim milk for 1 h to saturate unoccupied regions on the membrane. This was followed by adding the anti-NDV chicken serum or anti-*myc* monoclonal antibody (for fusion protein) onto the membrane and this was shaken for 1 h at room temperature. The membrane was then washed four times with TTBS washing solution (TBS containing 0.5% Tween 20), 5 to 10 min for each wash to remove the unbound antibodies. After washing, peroxidase-labelled antibody was added to react with the primary antibody and left shaking for another 1 h. The membrane was further washed four times with TTBS solution, each for 5 to 10 min, and lastly BCIP/NBT solution was added as substrate for the peroxidase. The molecular weight of NP and P proteins was about 55 kDa while the fusion form for both the NP and P proteins gave rise to an apparent molecular weight of about 60 kDa.

Purification of NP fusion protein using ProBond Column

Two hundred µl of LB medium containing 50 µg/ml ampicillin was cultured with 2 ml of overnight culture of transformant harbouring plasmid pTrcHis2-NP (carrying the NP insert without a stop codon), and the cells were grown to an OD_{600} of 0.6 to 0.8. Protein expression was then induced by adding 1 mM IPTG and the cells were grown for another 5 h. The cells were harvested by centrifugation at 2000 x*g* for 15 min at 4°C. The cell pellet was first resuspended in 10 ml of binding buffer (500 mM NaCl, 20 mM NaH_2PO_4, pH 7.8), then 100 µg/ml of lysozyme was added and incubated for 15 min on ice. The cells were lysed by sonication until the cell lysate is no longer viscous. The cell lysate was then treated with RNase and DNase I, both at a concentration of 5 µg/ml for 15 min at 30°C. The cell lysate was then centrifuged at 10,000 x*g* for 20 min to remove all the cell

debris. The supernatant was collected and passed through a 0.45 μm filter. This cell lysate was incubated with the ProBond resin (Invirogen, USA) for 30 min and then allowed to drip through the resin. The column was washed with 10 ml of washing buffer (50 mM Imidazole, 500 mM NaCl, 20 mM NaH_2PO_4, pH 6.0), and the proteins were then eluted with 5 ml of elution buffer (500 mM Imidazole, 500 mM NaCl, 20 mM NaH_2PO_4, pH 6.0). The elute was collected as 1 ml fractions. Samples from each fractions were analysed on 12% SDS-PAGE to check the purity of the protein.

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CLAIMS

1. Nucleotides encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).

2. The nucleotides as claimed in claim 1 characterised in that it has the following nucleotide sequence:

```
        10         20         30         40         50         60
ATGTCTTCCG TATTCGATGA ATACGAGCAG CTCCTCGCTG CTCAGACTCG CCCCAATGGA

        70         80         90        100        110        120
GCTCACGGAG GGGGAGAGAG AGGGAGCACT TTAAGAGTTG AGGTCCCAGT ATTCACTCTT

       130        140        150        160        170        180
AACAGTGACG ATCCAGAAGA TAGATGGAAT TTTGCGGTAT TCTGTCTTCG GATTGCTGTT

       190        200        210        220        230        240
AGCGAGGACG CCAACAAACC GCTCAGGCAA GGTGCTCTCA TATCCCTCCT GTGCTCCCAT

       250        260        270        280        290        300
TCTCAAGTGA TGAGGAACCA TGTTGCCCTT GCAGGAAAAC AGAATGAGGC TACACTGACT

       310        320        330        340        350        360
GTTCTTGAGA TCGATGGTTT TACCAGCAGC GTGCCTCAGT TCAACAACAG GAGTGGGGTG

       370        380        390        400        410        420
TCTGAGGAGA GAGCACAGAG ATTCATGGTG ATAGCAGGGT CTCTCCCTCG GGCGTGCAGT

       430        440        450        460        470        480
AACGGTACTC CGTTCGTCAC GGCTGGGGTT GAAGATGATG CACCAGAAGA TATCACTGAT

       490        500        510        520        530        540
ACTCTGGAAA GAATCCTGTC TATCCAGGCT CAGGTATGGG TCACAGTAGC GAAGGCCATG

       550        560        570        580        590        600
ACTGCATATG AGACAGCAGA TGAGTCGGAA ACAAGAAGAA TCAATAAGTA CATGCAGCAA

       610        620        630        640        650        660
GGCAGAGTCC AGAAGAAGTA CATCCTCCAC CCTGTATGCA GGAGTGCAAT TCAACTCACA

       670        680        690        700        710        720
ATCAGACATT CTCTGGCAGT CCGCATTTTC TTAGTTAGCG AGCTTAAGAG AGGCCGCAAT

       730        740        750        760        770        780
ACGGCAGGTG GGAGCTCCAC GTATTACAAC TTAGTAGGGG ATGTAGACTC ATACATCAGG

       790        800        810        820        830        840
AACACCGGAC TTACTGCATT CTTCCTTACA CTCAAATATG GAATTAATAC CAAGACATCA
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       850         860         870         880         890         900
GCCCTAGCAC TCAGCAGCCT CACAGGCGAT ATCCAAAAGA TGAAGCAGCT CATGCGTTTA

       910         920         930         940         950         960
TATCGGATGA AGGGAGAAAA TGCGCCGTAC ATGACATTGC TAGGTGACAG TGATCAGATG

       970         980         990        1000        1010        1020
AGCTTTGCAC CGGCTGAGTA TGCACAGCTT TATTCTTTTG CCATGGGCAT GGCATCAGTC

      1030        1040        1050        1060        1070        1080
TTAGATAAAG GAACTGGCAA ATACCAATTC GCCAGAGACT TCATGAGCAC ATCATTCTGG

      1090        1100        1110        1120        1130        1140
AGACTCGGGG TGGAGTATGC TCAGGCTCAG GGGAGTAGCA TCAACGAAGA CATGGCTGCT

      1150        1160        1170        1180        1190        1200
GAGCTAAAAC TAACCCCGGC AGCAAGAAGG GGCCTGGCAG CTGCTGCCCA ACGAGTGTCT

      1210        1220        1230        1240        1250        1260
GAGGAAACTG GCAGCGTGGA TATTCCTACT CAACAAGCCG GGGTCCTCAC TGGGCTCAGC

      1270        1280        1290        1300        1310        1320
GATGGAGGCC CCCGAGCCTC TCAGGGTGGA TCGAACAAGT CGCAAGGGCA ACCAGATGCC

      1330        1340        1350        1360        1370        1380
GGAGATGGGG AGACCCAATT CTTGGATTTG ATGAGAGCAG TGGCGAACAG CATGCGAGAA

      1390        1400        1410        1420        1430        1440
GCGCCAAACT CCGCACAGAG CACCACCCAC CCGGAACCCC CCCCGACTCC CGGGCCATCA

      1450        1460        1470        1480        1490        1500
CAAGATAACG ACACCGACTG GGGGTATTGA .......... .......... ..........
```

3. Nucleotides encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).

4. The nucleotides as claimed in claim 3 characterised in that it has the following nucleotide sequence:

```
        10          20          30          40          50          60
ATGGCCACCT TTACAGATGC GGAGATAGAT GATATATTTG AGACCAGTGG AACTGTCATT

        70          80          90         100         110         120
GACAGCATAA TTACGGCCCA GGGTAAATCA GCAGAGACTG TCGGAAGGAG CGCAATCCCA

       130         140         150         160         170         180
CAAGGCAAGA CCAAAGCGCT GAGCATAGCA TGGGAGAAGC ATGGGAGCAT CCAACCATCC

       190         200         210         220         230         240
ACCAGCCAGG ACAACCCCGA CCAACAGGAT AGACCAGACA AACAGCTATC CACACCTGAG

       250         260         270         280         290         300
CAGGCGACCC CACACAACAG CTCGCCAGCC ACATCCGCCG AACCGCTCCC CACTCAGGCC
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        310         320         330         340         350         360
GCAGGTGAGG CCGGCGACAC ACAGCTCAAG ACCGGAGCAA GCAACTCTCT TCTGTCTATG

        370         380         390         400         410         420
CTCGACAAGC TGAGCAATAA ACCATCTAAT GCTAAAAAGG GCCCATGGTC GAGTCCCCAG

        430         440         450         460         470         480
GAAGGATATC ATCAACCTCC GACCCAACAA CATGGGGATC AGCCGAACCG CGGAAACAGC

        490         500         510         520         530         540
CAGGAGAGGC TGCGGCACCA AGCCAAGGCC GCCCCTGGAA GCCGGGGCAC AGACGCGAGC

        550         560         570         580         590         600
ACAGCATATC ATGGACAATG GAAGGAGTCA CAACTATCAG CTGGTGCAAC CCCTCATGTG

        610         620         630         640         650         660
CTCCAATCAG GGCAGAGCCA AGACAGTACT CCTGTACCTG TGGATCATGT CCAGCCACCT

        670         680         690         700         710         720
GTCGACTTTG TGCAGGCGAT GATGACTATG ATGGAGGCGT TATCACAGAA GGTAAGTAAA

        730         740         750         760         770         780
GTCGACTATC AGCTAGACCT AGTCTTAAAG CAGACATCCT CCATCCCTAT GATGCGGTCT

        790         800         810         820         830         840
GAAATCCAAC AGCTAAAAAC ATCTGTTGCG GTCATGGAAG CTAATTTAGG CATGATGAAA

        850         860         870         880         890         900
ATTCTGGACC CTGGTTGTGC TAACATTTCA TCCTTAAGTG ATCTGCGGGC AGTCGCCCGG

        910         920         930         940         950         960
TCCCACCCAG TTTTAATTTC AGGCCCCGGA GATCCGTCCC CCTACGTGAC ACAAGGGGGT

        970         980         990        1000        1010        1020
GAGATGACAC TCAATAAACT CTCACAACCA GTACAACACC CTTCCGAGTT AATTAAATCT

       1030        1040        1050        1060        1070        1080
GCCACAGCGG GCGGACCTGA TATGGGAGTG GAAAAGGACA CTGTCCGTGC ATTGATCACC

       1090        1100        1110        1120        1130        1140
TCGCGCCCGA TGCATCCAAG CTCCTCAGCT AAGCTCCTGA GTAAGCTGGA TGCAGCCGGG

       1150        1160        1170        1180        1190        1200
TCGATTGAAG AGATCAGAAA GATCAAGCGC CTTGCACTAA ATGGCTAA.. ..........
```

5. The NP protein coded according to claim 1 or claim 2 characterised in that it has the following amino acid sequence:

```
 1   M   S   S   V   F   D   E   Y   E   Q   L   L   A   A   Q   T        16
    ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
    1           10          20          30          40

17   R   P   N   G   A   H   G   G   G   E   R   G   S   T   L   R       32
    CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
    50          60          70          80          90
```

```
33   V   E   V   P   V   F   T   L   N   S   D   D   P   E   D   R    48
     GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
       100         110         120         130         140

49   W   N   F   A   V   F   C   L   R   I   A   V   S   E   D   A    64
     TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
         150         160         170         180         190

65   N   K   P   L   R   Q   G   A   L   I   S   L   L   C   S   H    80
     AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
           200         210         220         230         240

81   S   Q   V   M   R   N   H   V   A   L   A   G   K   Q   N   E    96
     TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
             250         260         270         280

97   A   T   L   T   V   L   E   I   D   G   F   T   S   S   V   P   112
     GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
   290         300         310         320         330

113  Q   F   N   N   R   S   G   V   S   E   E   R   A   Q   R   F   128
     CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
       340         350         360         370         380

129  M   V   I   A   G   S   L   P   R   A   C   S   N   G   T   P   144
     ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG
         390         400         410         420         430

145  F   V   T   A   G   V   E   D   D   A   P   E   D   I   T   D   160
     TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT
           440         450         460         470         480

161  T   L   E   R   I   L   S   I   Q   A   Q   V   W   V   T   V   176
     ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA
             490         500         510         520

177  A   K   A   M   T   A   Y   E   T   A   D   E   S   E   T   R   192
     GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA
   530         540         550         560         570

193  R   I   N   K   Y   M   Q   Q   G   R   V   Q   K   K   Y   I   208
     AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC
       580         590         600         610         620

209  L   H   P   V   C   R   S   A   I   Q   L   T   I   R   H   S   224
     CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT
         630         640         650         660         670

225  L   A   V   R   I   F   L   V   S   E   L   K   R   G   R   N   240
     CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT
           680         690         700         710         720

241  T   A   G   G   S   S   T   Y   Y   N   L   V   G   D   V   D   256
     ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC
             730         740         750         760

257  S   Y   I   R   N   T   G   L   T   A   F   F   L   T   L   K   272
     TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA
   770         780         790         800         810

273  Y   G   I   N   T   K   T   S   A   L   A   L   S   S   L   T   288
     TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA
       820         830         840         850         860

289  G   D   I   Q   K   M   K   Q   L   M   R   L   Y   R   M   K   304
     GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG
         870         880         890         900         910
```

```
305  G   E   N   A   P   Y   M   T   L   L   G   D   S   D   Q   M    320
     GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG
               920         930         940         950         960

321  S   F   A   P   A   E   Y   A   Q   L   Y   S   F   A   M   G    336
     AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC
             970         980         990        1000

337  M   A   S   V   L   D   K   G   T   G   K   Y   Q   F   A   R    352
     ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA
    1010        1020        1030        1040        1050

353  D   F   M   S   T   S   F   W   R   L   G   V   E   Y   A   Q    368
     GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG
    1060        1070        1080        1090        1100

369  A   Q   G   S   S   I   N   E   D   M   A   A   E   L   K   L    384
     GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA
        1110        1120        1130        1140        1150

385  T   P   A   A   R   R   G   L   A   A   A   A   Q   R   V   S    400
     ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT
           1160        1170        1180        1190        1200

401  E   E   T   G   S   V   D   I   P   T   Q   Q   A   G   V   L    416
     GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC
             1210        1220        1230        1240

417  T   G   L   S   D   G   G   P   R   A   S   Q   G   G   S   N    432
     ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC
    1250        1260        1270        1280        1290

433  K   S   Q   G   Q   P   D   A   G   D   G   E   T   Q   F   L    448
     AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG
    1300        1310        1320        1330        1340

449  D   L   M   R   A   V   A   N   S   M   R   E   A   P   N   S    464
     GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
        1350        1360        1370        1380        1390

465  A   Q   S   T   T   H   P   E   P   P   P   T   P   G   P   S    480
     GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
           1400        1410        1420        1430        1440

481  Q   D   N   D   T   D   W   G   Y   *                            490
     CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
             1450        1460        1470
```

6. The P protein coded according to claim 3 or claim 4 characterised in that it has the following amino acid sequence:

```
 1   M   A   T   F   T   D   A   E   I   D   D   I   F   E   T   S    16
     ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
     1           10          20          30          40

17   G   T   V   I   D   S   I   I   T   A   Q   G   K   S   A   E    32
     GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
     50          60          70          80          90
```

```
33   T   V   G   R   S   A   I   P   Q   G   K   T   K   A   L   S      48
     ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
       100         110         120         130         140

49   I   A   W   E   K   H   G   S   I   Q   P   S   T   S   Q   D      64
     ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
         150         160         170         180         190

65   N   P   D   Q   Q   D   R   P   D   K   Q   L   S   T   P   E      80
     AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
           200         210         220         230         240

81   Q   A   T   P   H   N   S   S   P   A   T   S   A   E   P   L      96
     CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
             250         260         270         280

97   P   T   Q   A   A   G   E   A   G   D   T   Q   L   K   T   G     112
     CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
   290         300         310         320         330

113  A   S   N   S   L   L   S   M   L   D   K   L   S   N   K   P     128
     GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
       340         350         360         370         380

129  S   N   A   K   K   G   P   W   S   S   P   Q   E   G   Y   H     144
     TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
         390         400         410         420         430

145  Q   P   P   T   Q   Q   H   G   D   Q   P   N   R   G   N   S     160
     CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
           440         450         460         470         480

161  Q   E   R   L   R   H   Q   A   K   A   A   P   G   S   R   G     176
     CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
             490         500         510         520

177  T   D   A   S   T   A   Y   H   G   Q   W   K   E   S   Q   L     192
     ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA
   530         540         550         560         570

193  S   A   G   A   T   P   H   V   L   Q   S   G   Q   S   Q   D     208
     TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC
       580         590         600         610         620

209  S   T   P   V   P   V   D   H   V   Q   P   P   V   D   F   V     224
     AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG
         630         640         650         660         670

225  Q   A   M   M   T   M   M   E   A   L   S   Q   K   V   S   K     240
     CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA
           680         690         700         710         720

241  V   D   Y   Q   L   D   L   V   L   K   Q   T   S   S   I   P     256
     GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT
             730         740         750         760

257  M   M   R   S   E   I   Q   Q   L   K   T   S   V   A   V   M     272
     ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG
   770         780         790         800         810

273  E   A   N   L   G   M   M   K   I   L   D   P   G   C   A   N     288
     GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC
       820         830         840         850         860

289  I   S   S   L   S   D   L   R   A   V   A   R   S   H   P   V     304
     ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT
         870         880         890         900         910
```

```
305   L   I   S   G   P   G   D   P   S   P   Y   V   T   Q   G   G     320
      TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
                920         930         940         950         960

321   E   M   T   L   N   K   L   S   Q   P   V   Q   H   P   S   E     336
      GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
              970         980         990         1000

337   L   I   K   S   A   T   A   G   G   P   D   M   G   V   E   K     352
      TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
  1010        1020        1030        1040        1050

353   D   T   V   R   A   L   I   T   S   R   P   M   H   P   S   S     368
      GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
       1060        1070        1080        1090        1100

369   S   A   K   L   L   S   K   L   D   A   A   G   S   I   E   E     384
      TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
         1110        1120        1130        1140        1150

385   I   R   K   I   K   R   L   A   L   N   G   *                     396
      ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
            1160        1170        1180
```

7. A recombinant expression plasmid containing the NDV nucleocapsid gene as claimed in claim 1 or claim 2.

8. A recombinant expression plasmid containing the NDV phosphoprotein gene as claimed in claim 3 or claim 4.

9. The recombinant expression plasmid according to claim 7 which is the expression plasmid pTrcHis2-NP constructed by cloning the NDV nucleocapsid gene of claims 1 or 2 into vector pTrcHis2.

10. The recombinant expression plasmid according to claim 8 which is the expression plasmid pTrcHis2-P constructed by cloning the NDV phosphoprotein gene of claims 3 or 4 into vector pTrcHis2.

11. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 7 or claim 9.

12. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 8 or claim 10.

13. The transformed microorganism according to claim 11, which is the transformed *E. coli* TOP10 (pTrcHis2-NP) produced by introducing the recombinant expression plasmid of claim 7 or claim 9 into *E. coli* TOP10.

14. The transformed microorganism according to claim 12, which is the transformed *E. coli* (pTrcHis2-P) produced by introducing the recombinant expression plasmid of claim 8 or claim 10 into *E. coli* TOP 10.

15. A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13 characterised in that it has the following amino acid sequence:

```
  1  M  S  S  V  F  D  E  Y  E  Q  L  L  A  A  Q  T   16
ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
1          10          20          30          40

 17  R  P  N  G  A  H  G  G  G  E  R  G  S  T  L  R   32
CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
50          60          70          80          90

 33  V  E  V  P  V  F  T  L  N  S  D  D  P  E  D  R   48
GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
  100         110         120         130         140

 49  W  N  F  A  V  F  C  L  R  I  A  V  S  E  D  A   64
TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
    150         160         170         180         190

 65  N  K  P  L  R  Q  G  A  L  I  S  L  L  C  S  H   80
AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
       200         210         220         230         240

 81  S  Q  V  M  R  N  H  V  A  L  A  G  K  Q  N  E   96
TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
          250         260         270         280

 97  A  T  L  T  V  L  E  I  D  G  F  T  S  S  V  P  112
GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
290         300         310         320         330

113  Q  F  N  N  R  S  G  V  S  E  E  R  A  Q  R  F  128
CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
  340         350         360         370         380

129  M  V  I  A  G  S  L  P  R  A  C  S  N  G  T  P  144
ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG
    390         400         410         420         430

145  F  V  T  A  G  V  E  D  D  A  P  E  D  I  T  D  160
TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT
       440         450         460         470         480

161  T  L  E  R  I  L  S  I  Q  A  Q  V  W  V  T  V  176
ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA
          490         500         510         520
```

```
177   A   K   A   M   T   A   Y   E   T   A   D   E   S   E   T   R     192
      GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA
    530         540         550         560         570

193   R   I   N   K   Y   M   Q   Q   G   R   V   Q   K   K   Y   I     208
      ACA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC
      580         590         600         610         620

209   L   H   P   V   C   R   S   A   I   Q   L   T   I   R   H   S     224
      CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT
        630         640         650         660         670

225   L   A   V   R   I   F   L   V   S   E   L   K   R   G   R   N     240
      CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT
          680         690         700         710         720

241   T   A   G   G   S   S   T   Y   Y   N   L   V   G   D   V   D     256
      ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC
            730         740         750         760

257   S   Y   I   R   N   T   G   L   T   A   F   F   L   T   L   K     272
      TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA
    770         780         790         800         810

273   Y   G   I   N   T   K   T   S   A   L   A   L   S   S   L   T     288
      TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA
      820         830         840         850         860

289   G   D   I   Q   K   M   K   Q   L   M   R   L   Y   R   M   K     304
      GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG
        870         880         890         900         910

305   G   E   N   A   P   Y   M   T   L   L   G   D   S   D   Q   M     320
      GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG
          920         930         940         950         960

321   S   F   A   P   A   E   Y   A   Q   L   Y   S   F   A   M   G     336
      AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC
            970         980         990         1000

337   M   A   S   V   L   D   K   G   T   G   K   Y   Q   F   A   R     352
      ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA
    1010        1020        1030        1040        1050

353   D   F   M   S   T   S   F   W   R   L   G   V   E   Y   A   Q     368
      GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG
      1060        1070        1080        1090        1100

369   A   Q   G   S   S   I   N   E   D   M   A   A   E   L   K   L     384
      GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA
        1110        1120        1130        1140        1150

385   T   P   A   A   R   R   G   L   A   A   A   A   Q   R   V   S     400
      ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT
            1160        1170        1180        1190        1200

401   E   E   T   G   S   V   D   I   P   T   Q   Q   A   G   V   L     416
      GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC
            1210        1220        1230        1240

417   T   G   L   S   D   G   G   P   R   A   S   Q   G   G   S   N     432
      ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC
    1250        1260        1270        1280        1290

433   K   S   Q   G   Q   P   D   A   G   D   G   E   T   Q   F   L     448
      AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG
      1300        1310        1320        1330        1340
```

```
449  D   L   M   R   A   V   A   N   S   M   R   E   A   P   N   S   464
     GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
        1350        1360        1370        1380        1390

465  A   Q   S   T   T   H   P   E   P   P   P   T   P   G   P   S   480
     GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
          1400        1410        1420        1430        1440

481  Q   D   N   D   T   D   W   G   Y   *                           490
     CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
              1450        1460        1470
```

16. A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14 characterised in that it has the following amino acid sequence:

```
 1   M   A   T   F   T   D   A   E   I   D   D   I   F   E   T   S   16
     ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
     1           10          20          30          40

17   G   T   V   I   D   S   I   I   T   A   Q   G   K   S   A   E   32
     GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
     50          60          70          80          90

33   T   V   G   R   S   A   I   P   Q   G   K   T   K   A   L   S   48
     ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
       100         110         120         130         140

49   I   A   W   E   K   H   G   S   I   Q   P   S   T   S   Q   D   64
     ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
         150         160         170         180         190

65   N   P   D   Q   Q   D   R   P   D   K   Q   L   S   T   P   E   80
     AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
           200         210         220         230         240

81   Q   A   T   P   H   N   S   S   P   A   T   S   A   E   P   L   96
     CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
             250         260         270         280

97   P   T   Q   A   A   G   E   A   G   D   T   Q   L   K   T   G   112
     CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
   290         300         310         320         330

113  A   S   N   S   L   L   S   M   L   D   K   L   S   N   K   P   128
     GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
       340         350         360         370         380

129  S   N   A   K   K   G   P   W   S   S   P   Q   E   G   Y   H   144
     TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
         390         400         410         420         430

145  Q   P   P   T   Q   Q   H   G   D   Q   P   N   R   G   N   S   160
     CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
           440         450         460         470         480

161  Q   E   R   L   R   H   Q   A   K   A   A   P   G   S   R   G   176
     CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
             490         500         510         520
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177  T   D   A   S   T   A   Y   H   G   Q   W   K   E   S   Q   L   192
     ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA
530          540          550          560          570

193  S   A   G   A   T   P   H   V   L   Q   S   G   Q   S   Q   D   208
     TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC
580          590          600          610          620

209  S   T   P   V   P   V   D   H   V   Q   P   P   V   D   F   V   224
     AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG
630          640          650          660          670

225  Q   A   M   M   T   M   M   E   A   L   S   Q   K   V   S   K   240
     CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA
680          690          700          710          720

241  V   D   Y   Q   L   D   L   V   L   K   Q   T   S   S   I   P   256
     GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT
730          740          750          760

257  M   M   R   S   E   I   Q   Q   L   K   T   S   V   A   V   M   272
     ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG
770          780          790          800          810

273  E   A   N   L   G   M   M   K   I   L   D   P   G   C   A   N   288
     GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC
820          830          840          850          860

289  I   S   S   L   S   D   L   R   A   V   A   R   S   H   P   V   304
     ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT
870          880          890          900          910

305  L   I   S   G   P   G   D   P   S   P   Y   V   T   Q   G   G   320
     TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
920          930          940          950          960

321  E   M   T   L   N   K   L   S   Q   P   V   Q   H   P   S   E   336
     GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
970          980          990          1000

337  L   I   K   S   A   T   A   G   G   P   D   M   G   V   E   K   352
     TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
1010         1020         1030         1040         1050

353  D   T   V   R   A   L   I   T   S   R   P   M   H   P   S   S   368
     GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
1060         1070         1080         1090         1100

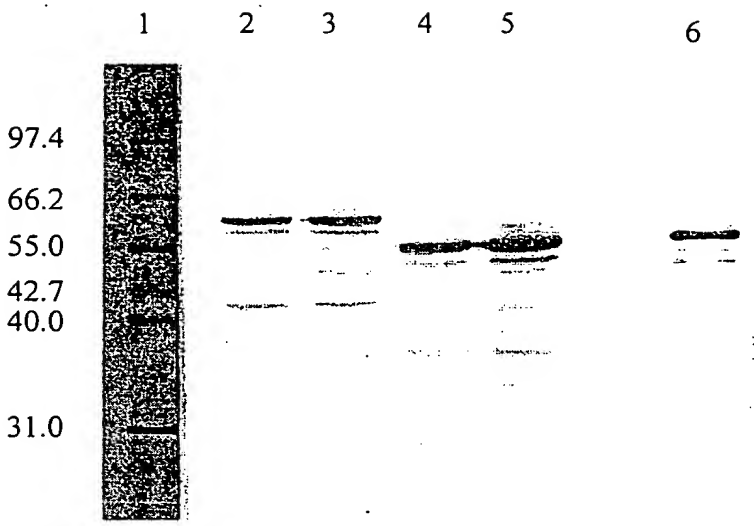
369  S   A   K   L   L   S   K   L   D   A   A   G   S   I   E   E   384
     TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
1110         1120         1130         1140         1150

385  I   R   K   I   K   R   L   A   L   N   G   *                   396
     ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
1160         1170         1180
```

ABSTRACT

Nucleotide Sequences of the Nucleocapsid (NP) and Phosphoprotein (P) Genes of a Malaysian Velogenic Newcastle Disease Virus Strain AF2240 and the Production of the NP and P Proteins in *Escherichia coli*

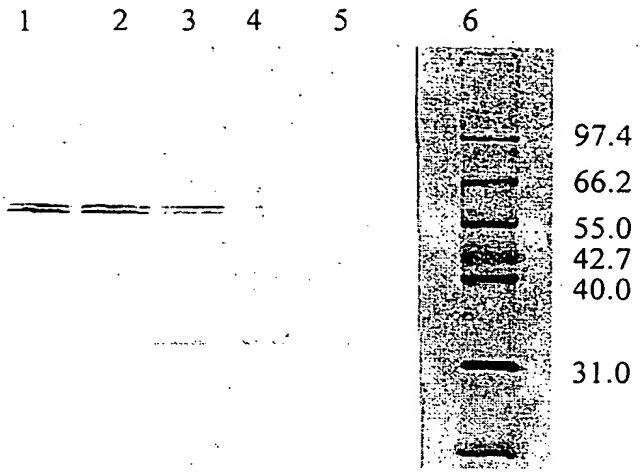
The present invention relates to nucleotide sequences encoding the nucleocapsid (NP) protein and phosphoprotein (P) of Newcastle disease virus (NDV) and the production of the corresponding proteins with recombinant plasmids bearing the nucleotide sequences in *Escherichia coli*.



Detection of NP protein with anti-NDV chicken serum

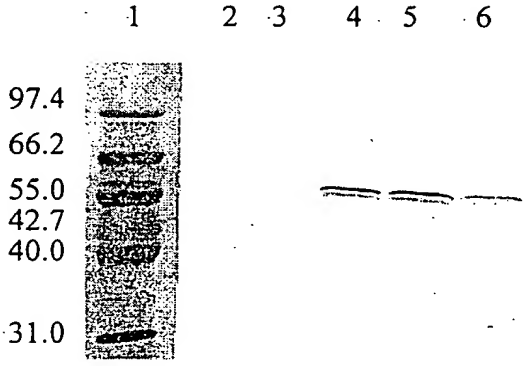
lanes:
1: Molecular mass standards expressed in kDa
2 & 3: NP fusion protein
4 & 5: NP non-fusion protein
6: NDV

Figure 1



Detection of P fusion protein with the anti-*Myc* monoclonal antibody

lanes:
1: Cells containing the recombinant P fusion plasmid after being induced with IPTG for 5 h
2: Cells containing the recombinant P fusion plasmid after being induced with IPTG for 3 h
3: Cells containing the recombinant P fusion plasmid after being induced with IPTG for 1 h
4: Cells containing the recombinant P fusion plasmid **before being induced with IPTG**
5: Cells harbouring empty vector
6: Molecular mass standards expressed in kDa



Detection of P non-fusion protein with anti-NDV chicken serum

lanes:
1: Molecular mass standards expressed in kDa
2: Cells harbouring empty vector
3: Cells containing the recombinant P non-fusion plasmid **before being induced with IPTG**
4: Cells containing the recombinant P non-fusion plasmid after being induced with IPTG for 2 h
5: Cells containing the recombinant P non-fusion plasmid after being induced with IPTG for 4 h
6: Cells containing the recombinant P non-fusion plasmid after being induced with IPTG for 6 h

Figure 2